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=> file biosis caba caplus lifesci medline
=> e bange franz christoph/au
E1            2     BANGE FRANZ C/AU
E2            1     BANGE FRANZ CH/AU
E3           33 --> BANGE FRANZ CHRISTOPH/AU
E4            5     BANGE G/AU
E5            2     BANGE G A/AU
E6            3     BANGE G G/AU
E7           42     BANGE G G J/AU
E8            1     BANGE GERARD G J/AU
E9           26     BANGE GERT/AU
E10          20     BANGE H W/AU
E11           2     BANGE HERMANN/AU
E12          17     BANGE HERMANN W/AU

=> s e1-e3
L1           36 ("BANGE FRANZ C"/AU OR "BANGE FRANZ CH"/AU OR "BANGE FRANZ CHRIS
                TOPH"/AU)
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           22 DUP REM L1 (14 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 22 ANSWERS - CONTINUE? Y/(N):y

L2   ANSWER 1 OF 22     MEDLINE on STN
AN   2007553213     MEDLINE <<LOGINID::20080825>>
DN   PubMed ID: 17868926
TI   Multidrug resistant tuberculosis in a 6 year old child.
AU   Suessmuth Sandra;   ***Bange Franz-Christoph***  ; Gappa Monika
CS   Department of Paediatric Pulmonology, Hannover Medical School, Hannover,
     Germany.
SO   Paediatric respiratory reviews, (2007 Sep) Vol. 8, No. 3, pp. 265-8.
     Electronic Publication: 2007-09-06.
     Journal code: 100898941. ISSN: 1526-0542.
CY   England: United Kingdom
DT   (CASE REPORTS)
     Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200801
ED   Entered STN: 18 Sep 2007
     Last Updated on STN: 23 Jan 2008
     Entered Medline: 22 Jan 2008
AB   The case is reported of a 6 year old girl whose mother had multidrug
     resistant tuberculosis (MDR TB).  The diagnostic algorithm and the pros
     and cons of treatment of MDR TB in a child are discussed.

L2   ANSWER 2 OF 22  LIFESCI    COPYRIGHT 2008 CSA on STN DUPLICATE 1
AN   2007:16893  LIFESCI <<LOGINID::20080825>>
TI   Successful treatment of post-kala-azar dermal leishmaniasis (PKDL) in a
     HIV infected patient with multiple relapsing leishmaniasis from Western
     Europe
AU   Rihl, Markus; Stoll, Matthias; Ulbricht, Kai;   ***Bange,***
  ***     Franz-Christoph***  ; Schmidt, Reinhold-Ernst
CS   Department of Rheumatology (OE 6850), Hannover Medical School (MHH), Carl-
     Neuberg-Str. 1, 30625 Hannover, Germany; E-mail: rihl.markus@mh-
     hannover.de
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SO Journal of Infection [J. Infect.], (20060700) vol. 53, no. 1, pp. e25-e27. ISSN: 0163-4453.
DT Journal
FS V
LA English
SL English
AB We present a 42-year-old man who was admitted with worsening of his general condition and facial skin lesions. He had previously been diagnosed with HIV infection and visceral leishmaniasis (VL). Diagnostic work-up revealed a new relapse of VL paralleled by the diagnosis of post-kala-azar dermal leishmaniasis (PKDL). The patient was treated with IV liposomal amphotericin B as well as sodium stibogluconate followed by oral hexadecylphosphocholine (miltefosine) over a period of 9 months. PKDL lesions began to disappear after 8 months of treatment. In addition, severe and relapsing VL so far remains in remission. This case demonstrates successful treatment of PKDL and relapsing VL in a Western European patient with HIV infection.

L2 ANSWER 3 OF 22 MEDLINE on STN
AN 2005528716 MEDLINE <<LOGINID::20080825>>
DN PubMed ID: 16206121
TI Candida kefyr as an emerging pathogen causing nosocomial bloodstream infections in neutropenic leukemia patients.
AU Reuter Christoph W M; Morgan Michael A; ***Bange Franz-Christoph*** ; Gunzer Florian; Eder Matthias; Hertenstein Bernd; Ganser Arnold
SO Clinical infectious diseases : an official publication of the Infectious Diseases Society of America, (2005 Nov 1) Vol. 41, No. 9, pp. 1365-6. Journal code: 9203213. E-ISSN: 1537-6591.
CY United States
DT Letter
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200607
ED Entered STN: 6 Oct 2005
Last Updated on STN: 14 Jul 2006
Entered Medline: 13 Jul 2006

L2 ANSWER 4 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:802885 CAPLUS <<LOGINID::20080825>>
DN 141:290059
TI A single nucleotide polymorphism in the narGHJI promoter for the detection and identification of Mycobacterium tuberculosis
IN ***Bange, Franz-christoph***
PA Artus- Gesellschaft Fuer Molekularbiologische Diagnostik Und Entwicklung Mbh, Germany
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004083459	A1	20040930	WO 2004-EP2911	20040319
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				

LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

DE	10313791	A1	20041007	DE 2003-10313791	20030320
AU	2004221678	A1	20040930	AU 2004-221678	20040319
CA	2519702	A1	20040930	CA 2004-2519702	20040319
EP	1606420	A1	20051221	EP 2004-721892	20040319
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK				
JP	2006521797	T	20060928	JP 2006-504758	20040319
US	20070015157	A1	20070118	US 2005-549495	20050915
IN	2005DN04651	A	20070817	IN 2005-DN4651	20051013
PRAI DE	2003-10313791	A	20030320		
WO	2004-EP2911	W	20040319		

AB A single nucleotide polymorphism (SNP) in the narGHJI operon of Mycobacterium tuberculosis is used to identify the bacterium in a biol. sample and to differentiate it from other members of the M. tuberculosis complex.

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 2

AN 2004:305778 BIOSIS <<LOGINID::20080825>>

DN PREV200400304326

TI A promoter mutation causes differential nitrate reductase activity of Mycobacterium tuberculosis and Mycobacterium bovis.

AU Stermann, Marion; Sedlacek, Ludwig; Maass, Silvia; ***Bange,*** *** Franz-Christoph*** [Reprint Author]

CS Dept Med Microbiol and Hosp Epidemiol, Hannover Med Sch, Carl Neuberg Str 1, D-30625, Hanover, Germany
bange@mikrobio.mh-hannover.de

SO Journal of Bacteriology, (May 2004) Vol. 186, No. 9, pp. 2856-2861. print.
CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 7 Jul 2004
Last Updated on STN: 7 Jul 2004

AB The recent publication of the genome sequence of Mycobacterium bovis showed >99.95% identity to M. tuberculosis. No genes unique to M. bovis were found. Instead numerous single-nucleotide polymorphisms (SNPs) were identified. This has led to the hypothesis that differential gene expression due to SNPs might explain the differences between the human and bovine tubercle bacilli. One phenotypic distinction between M. tuberculosis and M. bovis is nitrate reduction, which not only is an essential diagnostic tool but also contributes to mycobacterial pathogenesis. We previously showed that narGHJI encodes a nitrate reductase in both M. tuberculosis and M. bovis and that NarGHJI-mediated nitrate reductase activity was substantially higher in the human tubercle bacillus. In the present study we used a genetic approach to demonstrate that an SNP within the promoter of the nitrate reductase gene cluster narGHJI is responsible for the different nitrate reductase activity of M.

tuberculosis and M. bovis. This is the first example of an SNP that leads to differential gene expression between the human and bovine tubercle bacilli.

L2 ANSWER 6 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:627934 CAPLUS <<LOGINID::20080825>>
DN 139:174800
TI PCR-based detection of mycobacteria in clinical samples and identification of mycobacterial species by 16S-rRNA-gene polymorphism
IN ***Bange, Franz-Christoph*** ; Boettger, Erik Christian
PA Cytonet G.m.b.H. & Co. K.-G., Germany
SO Ger., 26 pp.
CODEN: GWXXAW
DT Patent
LA German
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI DE 10215238	C1	20030814	DE 2002-10215238	20020406
CA 2481517	A1	20031016	CA 2003-2481517	20030404
WO 2003085129	A1	20031016	WO 2003-EP3533	20030404
WO 2003085129	A8	20031231		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2003240448	A1	20031020	AU 2003-240448	20030404
EP 1495143	A1	20050112	EP 2003-729922	20030404
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
US 20060088833	A1	20060427	US 2005-510329	20051111
PRAI DE 2002-10215238	A	20020406		
WO 2003-EP3533	W	20030404		

AB The present invention concerns a mol.-biol. procedure for specific detection of mycobacteria. PCR based assay was developed for identification of the Mycobacterium tuberculosis complex and Mycobacterium avium from other mycobacteria in clin. samples. The assay uses amplification primers and oligonucleotide probes, which are specific to regions of 16S-rRNA-genes of mycobacteria.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 3
AN 2003:641546 CAPLUS <<LOGINID::20080825>>
DN 139:302761
TI Polymorphic nucleotide within the promoter of nitrate reductase (NarGHJI) is specific for Mycobacterium tuberculosis
AU Stermann, Marion; Bohrssen, Antje; Diephaus, Catharina; Maass, Silvia; ***Bange, Franz-Christoph***
CS Department of Medical Microbiology and Hospital Epidemiology, Medical School Hannover, Hannover, 30625, Germany

SO Journal of Clinical Microbiology (2003), 41(7), 3252-3259
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Mycobacterium tuberculosis rapidly reduces nitrate, leading to the accumulation of nitrite. This characteristic served for the past 40 yr to differentiate M. tuberculosis from other members of the Mycobacterium tuberculosis complex (MTBC), such as Mycobacterium bovis (non-BCG [referred to here as simply "M. bovis"]), Mycobacterium bovis BCG, Mycobacterium africanum, or Mycobacterium microti. Here, a narG deletion in M. tuberculosis showed that rapid nitrite accumulation of M. tuberculosis is mediated by narGHJI. Anal. of narG mutants of M. bovis and M. bovis BCG showed that, as in M. tuberculosis, nitrite accumulation was mediated by narGHJI, and no other nitrate reductase was involved. However, in contrast to M. tuberculosis, accumulation was delayed for several days. Comparison of the narGHJI promoter revealed that, at nucleotide -215 prior to the start codon of narG, M. tuberculosis carried a thymine residue, whereas the bovine mycobacteria carried a cytosine residue. Using LightCycler technol. we examd. 62 strains of M. tuberculosis, M. bovis, M. bovis BCG, M. microti, and M. africanum and demonstrated that this single nucleotide polymorphism was specific for M. tuberculosis. For further differentiation within the MTBC, we included, by using LightCycler technol., the previously described anal. of oxyR polymorphism, which is specific for the bovine mycobacteria, and the RD1 polymorphism, which is specific for M. bovis BCG. Based on these results, we suggest a LightCycler format for rapid and unambiguous diagnosis of M. tuberculosis, M. bovis, and M. bovis BCG.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 4
AN 2002:744654 CAPLUS <<LOGINID::20080825>>
DN 138:101518
TI Rapid-cycle PCR and fluorimetry for detection of mycobacteria
AU Lachnik, Jacqueline; Ackermann, Birgit; Bohrssen, Antje; Maass, Silvia; Diephaus, Catharina; Puncken, Axel; Stermann, Marion; ***Bange,*** *** Franz-Christoph***
CS Institute of Medical Microbiology, Medical School Hannover, Hannover, 30625, Germany
SO Journal of Clinical Microbiology (2002), 40(9), 3364-3373
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB In this study we used LightCycler PCR amplification and product detection by fluorescence resonance energy transfer probes to identify mycobacteria and differentiate between Mycobacterium tuberculosis complex, Mycobacterium avium, and other nontuberculous mycobacteria. Targeting the 16S rRNA gene, three different probes specific for mycobacteria, M. tuberculosis complex, and M. avium were constructed. As few as five genome copies of target nucleic acid were detected by the probes, illustrating the high sensitivity of the system. All 33 mycobacterial species tested but none of the closely related actinomycetes and other bacteria produced a specific fluorescence signal. A specificity of 100% was also demonstrated for the M. tuberculosis complex-specific probe and the M. avium-specific probe. Within 45 min, the LightCycler method

correctly detected mycobacteria and specifically identified M. tuberculosis complex and M. avium without any post-PCR sample manipulation. In view of future clin. studies, we also constructed and tested an internal control which could be used to assure successful amplification and detection of mycobacteria. Monitoring of PCR inhibition will be essential for evaluation of this system for direct detection of mycobacteria in clin. specimens. Finally, we tested our system on sputum seeded with mycobacteria and were able to detect as few as 10 organisms. At present, this system is the fastest available method for identification and differentiation of mycobacteria from culture-pos. specimens and offers an excellent alternative to previously established nucleic acid amplification-based techniques for the diagnostic mycobacterial lab.

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 5

AN 2002:144790 BIOSIS <<LOGINID::20080825>>

DN PREV200200144790

TI Dependence of Mycobacterium bovis BCG on anaerobic nitrate reductase for persistence is tissue specific.

AU Fritz, Christian; Maass, Silvia; Kreft, Andreas; ***Bange,*** *** Franz-Christoph*** [Reprint author]

CS Institute fuer Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany
bange@mikrobio.mh-hannover.de

SO Infection and Immunity, (January, 2002) Vol. 70, No. 1, pp. 286-291. print.
CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

ED Entered STN: 14 Feb 2002
Last Updated on STN: 26 Feb 2002

AB Mycobacterium bovis BCG, the only presently available vaccine against tuberculosis, was obtained from virulent M. bovis after serial passages in vitro. The vaccine strain retained at least some of its original virulence, as it persists in immune-competent hosts and occasionally may cause fatal disease in immune-deficient hosts. Mycobacterial persistence in vivo is thought to depend on anaerobic metabolism, an apparent paradox since all mycobacteria are obligate aerobes. Here we report that M. bovis BCG lacking anaerobic nitrate reductase (NarGHJI), an enzyme essential for nitrate respiration, failed to persist in the lungs, liver, and kidneys of immune-competent (BALB/c) mice. In immune-deficient (SCID) mice, however, bacilli caused chronic infection despite disruption of narG, even if growth of the mutant was severely impaired in lungs, liver, and kidneys. Persistence and growth of BCG in the spleens of either mouse strain appeared largely unaffected by lack of anaerobic nitrate reductase, indicating that the role of the enzyme in pathogenesis is tissue specific. These data suggest first that anaerobic nitrate reduction is essential for metabolism of M. bovis BCG in immune-competent but not immune-deficient mice and second that its role in mycobacterial disease is tissue specific, both of which are observations with important implications for pathogenesis of mycobacteria and vaccine development.

L2 ANSWER 10 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN

AN 2001:359658 BIOSIS <<LOGINID::20080825>>

DN PREV200100359658
TI Lack of transmission of Mycobacterium abscessus among patients with cystic fibrosis attending a single clinic.
AU ***Bange, Franz-Christoph*** [Reprint author]; Brown, Barbara A.; Smaczny, Christina; Wallace, Richard J., Jr.; Bottger, Erik C.
CS Institut fuer Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany
bange@mikrobio.mh-hannover.de
SO Clinical Infectious Diseases, (1 June, 2001) Vol. 32, No. 11, pp. 1648-1650. print.
CODEN: CIDIEL. ISSN: 1058-4838.
DT Article
LA English
ED Entered STN: 2 Aug 2001
Last Updated on STN: 19 Feb 2002
AB We retrospectively analyzed 1062 respiratory specimens from 214 patients with cystic fibrosis, of whom 5 patients had 36 cultures positive for M. abscessus. Results of molecular typing demonstrated that each of these 5 patients carried a single unique strain (genotype), which suggests that it may not be necessary to segregate patients with CF who are colonized or infected with M. abscessus from those who are not.

L2 ANSWER 11 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 6
AN 2000:182005 BIOSIS <<LOGINID::20080825>>
DN PREV200000182005
TI Anaerobic nitrate reductase (narGHJI) activity of Mycobacterium bovis BCG in vitro and its contribution to virulence in immunodeficient mice.
AU Weber, Isabel; Fritz, Christian; Ruttkowski, Silvia; Kreft, Andreas; ***Bange, Franz-Christoph*** [Reprint author]
CS Institute of Medical Microbiology, Medical School Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany
SO Molecular Microbiology, (March, 2000) Vol. 35, No. 5, pp. 1017-1025. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 11 May 2000
Last Updated on STN: 4 Jan 2002
AB Mycobacterium tuberculosis and Mycobacterium bovis cause tuberculosis, which is responsible for the deaths of more people each year than any other bacterial infectious disease. Disseminated disease with Mycobacterium bovis BCG, the only currently available vaccine against tuberculosis, occurs in immunocompetent and immunodeficient individuals. Although mycobacteria are obligate aerobes, they are thought to face an anaerobic environment during infection, notably inside abscesses and granulomas. The purpose of this study was to define a metabolic pathway that could allow mycobacteria to exist under these conditions. Recently, the complete genome of M. tuberculosis has been sequenced, and genes homologous to an anaerobic nitrate reductase (narGHJI), an enzyme allowing nitrate respiration when oxygen is absent, were found. Here, we show that the narGHJI cluster of M. tuberculosis is functional as it conferred anaerobic nitrate reductase activity to Mycobacterium smegmatis. A narG mutant of M. bovis BCG was generated by targeted gene deletion. The mutant lacked the ability to reduce nitrate under anaerobic conditions. Both mutant and M. bovis BCG wild type grew equally well under aerobic conditions in vitro. Histology of immunodeficient mice (SCID) infected

with M. bovis BCG wild type revealed large granulomas teeming with acid-fast bacilli; all mice showed signs of clinical disease after 50 days and succumbed after 80 days. In contrast, mice infected with the mutant had smaller granulomas containing fewer bacteria; these mice showed no signs of clinical disease after more than 200 days. Thus, it seems that nitrate respiration contributes significantly to virulence of M. bovis BCG in immunodeficient SCID mice.

L2 ANSWER 12 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 1999:530699 BIOSIS <<LOGINID::20080825>>
DN PREV199900530699
TI Recovery of mycobacteria from patients with cystic fibrosis.
AU ***Bange, Franz-Christoph*** [Reprint author]; Kirschner, Philip; Boettger, Eric C.
CS Institute fuer Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany
SO Journal of Clinical Microbiology, (Nov., 1999) Vol. 37, No. 11, pp. 3761-3763. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 10 Dec 1999
Last Updated on STN: 10 Dec 1999
AB Despite decontamination, overgrowth by pseudomonads renders cultural isolation of mycobacteria from respiratory specimens of patients with cystic fibrosis (CF) difficult or impossible. We performed a prospective study by comparing levels of reduction of overgrowth and recovery of mycobacteria using either pretreatment with N-acetyl-L-cysteine (NALC)-NaOH alone or pretreatment with NALC-NaOH and then with oxalic acid. From 406 specimens of 148 CF patients, 11 specimens were positive for mycobacteria, 5 of which grew mycobacteria after decontamination by either procedure. Three specimens grew mycobacteria only after decontamination with NALC-NaOH, whereas three specimens grew mycobacteria only after treatment with NALC-NaOH followed by oxalic acid but were overgrown after decontamination with NALC-NaOH. Thus, inactivation of mycobacteria by the more aggressive oxalic acid treatment offsets its beneficial effect of reducing the proportion of cultures overgrown with microorganisms other than mycobacteria.

L2 ANSWER 13 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 7
AN 1996:268407 BIOSIS <<LOGINID::20080825>>
DN PREV199698824536
TI Leucine auxotrophy restricts growth of Mycobacterium bovis BCG in macrophages.
AU ***Bange, Franz-Christoph*** ; Brown, Amanda M.; Jacobs, William R., Jr. [Reprint author]
CS Howard Hughes Med. Inst., Dep. Microbiol. Immunol., Albert Einstein Coll. Med. Yeshiva Univ., 1300 Morris Park Ave., Bronx, NY 10461, USA
SO Infection and Immunity, (1996) Vol. 64, No. 5, pp. 1794-1799.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 10 Jun 1996
Last Updated on STN: 10 Jun 1996
AB The ability of slow-growing mycobacteria to replicate within host

mononuclear phagocytes is thought to be central to the pathogenesis of mycobacterial infection. However, because of the lack of a mycobacterial mutant defective for intracellular replication, it has not been possible to test this hypothesis directly. Previously, we showed that a BCG leucine auxotroph with a transposon disruption of the leuD gene is unable to grow in mice. Here we demonstrate that this mutant is also incapable of replicating within cultured macrophages in vitro. Complementation of the leuD mutation with the leuCD genes of Escherichia coli restored wild-type levels of growth in macrophages, establishing that the defect for intracellular replication was due to leucine auxotrophy per se and not to a polar effect of the transposon insertion on an adjacent gene. These results suggest that the inability of the leucine auxotroph to grow in mice was due to its sequestration, after phagocytosis, in an intracellular compartment from which it could not obtain leucine.

L2 ANSWER 14 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 1996:259148 BIOSIS <<LOGINID::20080825>>
DN PREV199698815277
TI Intracellular replication of leucine auxotrophs of slow-growing mycobacteria.
AU ***Bange, Franz-Christoph*** ; Jacobs, William R., Jr.
CS Howard Hughes Med. Inst., Albert Einstein Coll. Med., Yeshiva Univ., 1300 Morris Park Avenue, Bronx, NY 10461, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (1996) Vol. 96, No. 0, pp. 131.
Meeting Info.: 96th General Meeting of the American Society for Microbiology. New Orleans, Louisiana, USA. May 19-23, 1996.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 31 May 1996
Last Updated on STN: 31 May 1996

L2 ANSWER 15 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 8
AN 1995:108753 BIOSIS <<LOGINID::20080825>>
DN PREV199598123053
TI Up-regulation of keratin 17 expression in human HaCaT keratinocytes by interferon-gamma.
AU Bonnekoh, Bernd [Reprint author]; Huerkamp, Christina; Wevers, Andrea; Geisel, Jurgen; Sebok, Bela; ***Bange, Franz-C.*** ; Greenhalgh, David A.; Bottger, Erik C.; Krieg, Thomas; Mahrle, Gustav
CS Dep. Cell Biology, Room 132C, Baylor Coll. Med., One Baylor Plaza, Houston, TX 77030, USA
SO Journal of Investigative Dermatology, (1995) Vol. 104, No. 1, pp. 58-61.
CODEN: JIDEAE. ISSN: 0022-202X.
DT Article
LA English
ED Entered STN: 13 Mar 1995
Last Updated on STN: 13 Mar 1995
AB The immortalized human keratinocyte cell line Ha-CaT was used to assess the effect of interferon-gamma (IFN-gamma) on expression of keratin K17. Both IFN-gamma and K17 have been implicated in the pathophysiology of psoriasis. Western and quantitative enzyme-linked immunosorbent assay analyses demonstrated increasing induction of K17 protein by 48 h exposure

to IFN-gamma at concentrations of 10, 50, and 250 U/ml. At 50 U/ml IFN-gamma, immunohistochemical analysis revealed numerous K17-positive foci, whereas in situ hybridization demonstrated K17 message in the majority of cells. In addition, at low (5 U/ml) concentrations of IFN-gamma, cell proliferation and protein synthesis decreased, as determined by 3H-thymidine labeling and 14C-amino acid uptake. These data suggest that aberrant K17 expression observed in psoriatic lesions may be a consequence of EFN-gamma overexpression, and that the HaCaT cell line may be a useful in vitro model system to elucidate the underlying mechanisms.

L2 ANSWER 16 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 9
AN 1994:109697 BIOSIS <<LOGINID::20080825>>
DN PREV199497122697
TI IFP 35 is an interferon-induced leucine zipper protein that undergoes interferon-regulated cellular redistribution.
AU ***Bange, Franz-Christoph*** ; Vogel, Ulrich; Flohr, Thomas; Kiekenbeck, Monika; Denecke, Bernd; Boettger, Erick C. [Reprint author]
CS Inst. Med. Mikrobiologie, Med. Hochschule Hannover, 30623 Hannover, Germany
SO Journal of Biological Chemistry, (1994) Vol. 269, No. 2, pp. 1091-1098. CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS EMBL-P80217; Genbank-P80217
ED Entered STN: 14 Mar 1994
Last Updated on STN: 15 Mar 1994
AB We have isolated a new human cDNA, named IFP 35, whose expression is regulated by interferons (IFN). Induction of IFP 35 mRNA in HeLa cells by IFN is due, at least in part, to increased transcription. In response to IFN treatment, the expression of IFP 35 mRNA is seen in a wide range of different cell types, including fibroblasts, macrophages, and epithelial cells. The cDNA sequence encodes a 282-amino acid protein with a deduced molecular mass of 31,130 Da. In vitro translation of mRNA obtained by both in vitro transcription and hybrid selection resulted in the synthesis of a 35kDa protein. Antisera raised against IFP 35 recognized a protein with an apparent molecular mass of 35 kDa in HeLa cells. Amino acid sequence analysis revealed a leucine zipper motif in an alpha-helical configuration at the extreme amino terminus of IFP 35. Notably IFP 35 is a unique novel leucine zipper protein in that it lacks a basic domain critical for DNA binding. IFP 35 can specifically form homodimers in vitro. Western blot analysis of fractionated cell extracts indicates increased nuclear localization following IFN treatment.

L2 ANSWER 17 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 10
AN 1994:159143 BIOSIS <<LOGINID::20080825>>
DN PREV199497172143
TI Genetic alterations in streptomycin-resistant Mycobacterium tuberculosis: Mapping of mutations conferring resistance.
AU Meier, Albrecht; Kirschner, Philip; ***Bange, Franz-Christoph*** ; Vogel, Ulrich; Boettger, Erik C. [Reprint author]
CS Institut Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Konstanty-Gutschow-Strasse 8, 30623 Hannover, Germany
SO Antimicrobial Agents and Chemotherapy, (1994) Vol. 38, No. 2, pp. 228-233. CODEN: AMACCQ. ISSN: 0066-4804.

DT Article
LA English
ED Entered STN: 8 Apr 1994
Last Updated on STN: 10 Apr 1994
AB We report on the identification of mutations associated with streptomycin resistance in Mycobacterium tuberculosis. Two isolates (3656 and 3976) showed a wild-type ribosomal protein, S12, but exhibited a single point mutation at 16S rRNA position 491 (C fwdarw T) or 512 (C fwdarw T), respectively. Sequence analysis of a third isolate (2438) revealed a single base change at 16S rRNA position 904 (A fwdarw G). This position is equivalent to invariant position 913 of the Escherichia coli 16S rRNA gene, an A fwdarw G transition of which has been shown previously to impair streptomycin binding and streptomycin-induced misreading in vitro. Surprisingly, strain 2438 harbors an additional mutation in the ribosomal protein S12 (Lys-88 fwdarw Gln).

L2 ANSWER 18 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 11
AN 1993:454307 BIOSIS <<LOGINID::20080825>>
DN PREV199396099207
TI The gene encoding IFP 53-tryptophanyl-tRNA synthetase is regulated by the gamma-interferon activation factor.
AU Strehlow, Inga; Seegert, Dirk; Frick, Christiane; ***Bange,*** *** Franz-Christoph*** ; Schindler, Christian; Boettger, Erik C.; Decker, Thomas [Reprint author]
CS Fraunhofer Inst. Toxicol. and Mol. Biol., Nikolai-Fuchsstrasse 1, D-3000 Hannover 61, Germany
SO Journal of Biological Chemistry, (1993) Vol. 268, No. 22, pp. 16590-16595. CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 5 Oct 1993
Last Updated on STN: 3 Jan 1995
AB We have obtained genomic DNA encoding the interferon-gamma (IFN-gamma)-inducible IFP 53/tryptophanyl-tRNA synthetase. Comparison with several different IFP 53 cDNA clones revealed a complex pattern of alternatively spliced 5'-untranslated regions. The interferonresponsive region within the IFP 53 promoter was found to contain a gamma-interferon activation site (GAS) but not the interferon-stimulated response element and to bind the gamma-interferon activation factor (GAF). GAF-GAS complexes contained the IFN-regulated 91-kDa protein. Competition experiments defined the GAS boundaries and showed that GAF binding to the IFP 53 GAS could be prevented by an excess of the IFN-gamma response regions of several other IFN-gamma-inducible genes. We thus provide evidence for a central role of GAS-GAF in gene transcription mediated by IFN-gamma and suggest a consensus sequence defining more precisely the requirements for GAF binding to DNA.

L2 ANSWER 19 OF 22 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 1993:587121 BIOSIS <<LOGINID::20080825>>
DN PREV199497006491
TI Genotypic identification of mycobacteria by nucleic acid sequence determination: Report of a 2-year experience in a clinical laboratory.
AU Kirschner, Philip; Springer, Burkhard; Vogel, Ulrich; Meier, Albrecht; Wrede, Annette; Kiekenbeck, Monika; ***Bange, Franz-Christoph*** ; Boettger, Erik C. [Reprint author]

CS Inst. Med. Mikrobiol., Med. Hochschule Hannover, Konstanty-Gutschow-Str. 8, 30623 Hannover, Germany
SO Journal of Clinical Microbiology, (1993) Vol. 31, No. 11, pp. 2883-2889. CODEN: JCMIDW. ISSN: 0095-1137.
DT Article
LA English
ED Entered STN: 28 Dec 1993
Last Updated on STN: 28 Dec 1993
AB Clinical isolates of Mycobacterium spp. were identified by direct sequence determination of 16S rRNA gene fragments amplified by polymerase chain reaction. Identification was based on a hypervariable region within the 16S rRNA gene in which mycobacterial species are characterized by species-specific nucleotide sequences. A manually aligned data base including the signature sequences of 52 species of mycobacteria easily allowed rapid and correct identification. The results of this study demonstrate that polymerase chain reaction-mediated direct sequence determination can be used as a rapid and reliable method for the identification of mycobacteria in the clinical laboratory. In addition, the prompt recognition of previously undescribed species is now feasible.

L2 ANSWER 20 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1994:70337 CAPLUS <<LOGINID::20080825>>
DN 120:70337
OREF 120:12531a,12534a
TI Genotypic identification of mycobacteria by nucleic acid sequence determination: Report of a 2-year experience in a clinical laboratory
AU Kirschner, Philip; Springer, Burkhard; Vogel, Ulrich; Meier, Albrecht; Wrede, Annette; Kiekenbeck, Monika; ***Bange, Franz Christoph*** ; Boettger, Erik
CS Inst. Med. Mikrobiol., Med. Hochsch. Hannover, Hannover, 30623, Germany
SO Journal of Clinical Microbiology (1993), 31(11), 2882-9 CODEN: JCMIDW; ISSN: 0095-1137
DT Journal
LA English
AB Clin. isolates of Mycobacterium spp. were identified by direct sequence detn. of 16S rRNA gene fragments amplified by polymerase chain reaction. Identification was based on a hypervariable region within the 16S rRNA gene in which mycobacterial species are characterized by species-specific nucleotide sequences. A manually aligned data base including the signature sequences of 52 species of mycobacteria easily allowed rapid and correct identification. The results of this study demonstrate that polymerase chain reaction-mediated direct sequence detn. can be used as a rapid and reliable method for the identification of mycobacteria in the clin. lab. In addn., the prompt recognition of previously undescribed species is now feasible.

L2 ANSWER 21 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1993:20706 CAPLUS <<LOGINID::20080825>>
DN 118:20706
OREF 118:3889a,3892a
TI Depletion of tryptophan is not involved in expression of tryptophanyl-tRNA synthetase mediated by interferon
AU Flohr, Thomas; ***Bange, Franz Christoph*** ; Von Euch, Andreas; Kiekenbeck, Monika; Boettger, Erik C.
CS Inst. Med. Microbiol., Med. Sch. Hannover, Hannover, 3000/61, Germany
SO Infection and Immunity (1992), 60(10), 4418-21 CODEN: INFIBR; ISSN: 0019-9567

DT Journal
LA English
AB Gamma interferon (IFN-.gamma.) affects tryptophan metab. by mediating the expression of indoleamine 2,3-dioxygenase and tryptophanyl-tRNA synthetase. In the present study, the role of indoleamine 2,3-dioxygenase-mediated tryptophan depletion in the induction of tryptophanyl-tRNA synthetase by IFN-.gamma. was investigated. The addn. of excess tryptophan to the culture medium did not affect the induction of tryptophanyl-tRNA synthetase by IFN-.gamma., indicating that tryptophan degrdn. is not directly involved in the IFN-.gamma.-mediated expression of tryptophanyl-tRNA synthetase.

L2 ANSWER 22 OF 22 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1992:210117 CAPLUS <<LOGINID::20080825>>
DN 116:210117
OREF 116:35495a,35498a
TI An interferon-induced protein with release factor activity is a tryptophanyl-tRNA synthetase
AU ***Bange, Franz C.*** ; Flohr, Thomas; Buwitt, Ute; Boettger, Erik C.
CS Inst. Med. Microbiol., Med. Sch. Hannover, Hannover, Germany
SO FEBS Letters (1992), 300(2), 162-6
    CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB Interferon-.gamma. induces expression of a protein termed IFP 53 according to its mol. wt. of 53 kDa. IFP 53 shows significant sequence homol. to rabbit peptide chain release factor as well as to bovine tryptophanyl-tRNA synthetase. IFP 53 has been shown to possess release factor activity for the UGA stop codon. Here, by using a recombinant IFP 53 fusion protein, it is demonstrated that IFP 53 tryptophanylates tRNA. These data indicate that IFP 53 is a protein with 2 activities, peptide chain termination and aminoacylation.

=> s tuberculosis/ti and primer? and amplif?
L3 880 TUBERCULOSIS/TI AND PRIMER? AND AMPLIF?

=> s l3 and narGHJI
L4 1 L3 AND NARGHJI

=> d

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:802885 CAPLUS <<LOGINID::20080825>>
DN 141:290059
TI A single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium ***tuberculosis***
IN Bange, Franz-christoph
PA Artus- Gesellschaft Fuer Molekularbiologische Diagnostik Und Entwicklung Mbh, Germany
SO PCT Int. Appl., 46 pp.
    CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

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PI   WO 2004083459         A1    20040930    WO 2004-EP2911          20040319
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE,
             GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
             LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO,
             NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ,
             TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,
             BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
             ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI,
             SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN,
             TD, TG
     DE 10313791           A1    20041007    DE 2003-10313791        20030320
     AU 2004221678         A1    20040930    AU 2004-221678          20040319
     CA 2519702            A1    20040930    CA 2004-2519702         20040319
     EP 1606420            A1    20051221    EP 2004-721892          20040319
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK
     JP 2006521797         T     20060928    JP 2006-504758          20040319
     US 20070015157        A1    20070118    US 2005-549495          20050915
     IN 2005DN04651        A     20070817    IN 2005-DN4651          20051013
PRAI DE 2003-10313791      A     20030320
     WO 2004-EP2911        W     20040319
RE.CNT  6     THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> s tuberculosis and primer? and amplif? and narGHJI
L5            1 TUBERCULOSIS AND PRIMER? AND AMPLIF? AND NARGHJI

=> d

L5   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2008 ACS on STN
AN   2004:802885  CAPLUS <<LOGINID::20080825>>
DN   141:290059
TI   A single nucleotide polymorphism in the   ***narGHJI***   promoter for the
     detection and identification of Mycobacterium   ***tuberculosis***
IN   Bange, Franz-christoph
PA   Artus- Gesellschaft Fuer Molekularbiologische Diagnostik Und Entwicklung
     Mbh, Germany
SO   PCT Int. Appl., 46 pp.
     CODEN: PIXXD2
DT   Patent
LA   German
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.         DATE
     ---------------     ----   --------    --------------------    --------
PI   WO 2004083459         A1    20040930    WO 2004-EP2911          20040319
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE,
             GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
             LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO,
             NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ,
             TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,
             BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
             ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI,
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SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

DE	10313791	A1	20041007	DE 2003-10313791	20030320
AU	2004221678	A1	20040930	AU 2004-221678	20040319
CA	2519702	A1	20040930	CA 2004-2519702	20040319
EP	1606420	A1	20051221	EP 2004-721892	20040319
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK				
JP	2006521797	T	20060928	JP 2006-504758	20040319
US	20070015157	A1	20070118	US 2005-549495	20050915
IN	2005DN04651	A	20070817	IN 2005-DN4651	20051013
PRAI DE	2003-10313791	A	20030320		
WO	2004-EP2911	W	20040319		

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s tuberculosis and narGHJI
L6 29 TUBERCULOSIS AND NARGHJI

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 9 DUP REM L6 (20 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L7 ANSWER 1 OF 9 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 1
AN 2008:389140 BIOSIS <<LOGINID::20080825>>
DN PREV200800389139
TI A simple whole cell based high throughput screening protocol using Mycobacterium bovis BCG for inhibitors against dormant and active tubercle bacilli.
AU Khan, Arshad; Sarkar, Dhiman [Reprint Author]
CS Natl Chem Lab, CombiChem Bio Resource Ctr, Dr Homi Bhabha Rd, Pune 411008, Maharashtra, India
aa.khan@ncl.res.in; dhimansarkar77@gmail.com
SO Journal of Microbiological Methods, (APR 2008) Vol. 73, No. 1, pp. 62-68. CODEN: JMIMDQ. ISSN: 0167-7012.
DT Article
LA English
ED Entered STN: 16 Jul 2008
Last Updated on STN: 16 Jul 2008
AB This study aimed at developing a whole cell based high throughput screening protocol to identify inhibitors against both active and dormant tubercle bacilli. A respiratory type of nitrate reductase (***NarGHJI***), which was induced during dormancy, could reflect the viability of dormant bacilli of Mycobacterium bovis BCG in microplate adopted model of in vitro dormancy. Correlation between reduction in viability and nitrate reductase activity was seen clearly when dormant stage inhibitor metronidazole and itaconic anhydride were applied in this in vitro microplate model. Active replicating stage could also be monitored in the same assay by measuring the A(620) of the culture. MIC values of 0.08, 0.075, 0.3 and 3.0 mu g/ml, determined through monitoring A(620) in this assay for rifampin, isoniazid, streptomycin and ethambutol

respectively, were well in agreement with previously reported by BACTEC and Bio-Siv assays. S/N ratio and Z' factor for the assay were 8.5 and 0.81 respectively which indicated the robustness of the protocol. Altogether the assay provides an easy, inexpensive, rapid, robust and high content screening too] to search novel antitubercular molecules against both active and dormant bacilli. (C) 2008 Elsevier B.V. All rights reserved.

AB. . . high throughput screening protocol to identify inhibitors against both active and dormant tubercle bacilli. A respiratory type of nitrate reductase (***NarGHJI***), which was induced during dormancy, could reflect the viability of dormant bacilli of Mycobacterium bovis BCG in microplate adopted model. . .

IT Major Concepts
Pharmacology; Infection

IT Diseases
tuberculosis : bacterial disease, drug therapy
Tuberculosis (MeSH)

IT Chemicals & Biochemicals
rifampin: enzyme inhibitor-drug, antiinfective-drug, antibacterial-drug; nitrate reductase [EC 1.7.99.4]; streptomycin: enzyme inhibitor-drug, antiinfective-drug, antibacterial-drug; isoniazid:. . .

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium ***tuberculosis*** (species): pathogen
Mycobacterium bovis (species): strain-BCG

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L7 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 2

AN 2005:984897 CAPLUS <<LOGINID::20080825>>

DN 144:289142

TI Molecular evolutionary history of tubercle bacilli assessed by study of the polymorphic nucleotide within the nitrate reductase (***narGHJI***) operon promoter

AU Goh, Khye Seng; Rastogi, Nalin; Berchel, Mylene; Huard, Richard C.; Sola, Christophe

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Pointe-a-Pitre, Guam

SO Journal of Clinical Microbiology (2005), 43(8), 4010-4014
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB A well-characterized collection of Mycobacterium ***tuberculosis*** complex (MTC) isolates, representing all known subspecies as well as some relevant genotypic families of M. ***tuberculosis*** , was analyzed for the newly discovered ***narGHJI*** -215 C-to-T promoter single-nucleotide polymorphism (SNP). This point mutation has been shown in earlier studies to be responsible for the differential nitrate reductase activity of M. ***tuberculosis*** vs. M. bovis. As previously defined by the presence or the absence of the TbD1 genetic locus, the group included both the "modern" W-Beijing, Haarlem, and

Central-Asian1 (CAS1) families as well as the "ancestral" East-African-Indian (EAI) clade. Interestingly, among "modern" M. ***tuberculosis*** isolates, those previously classified as Principal Genetic Group 1 (PGG1) organisms by katG463-gyrA95 polymorphism anal. did not present the two-banded ***narGHJI*** restriction fragment length polymorphism anal. of PCR products pattern common to the other PGG1 MTC members, including the "ancestral" M. ***tuberculosis*** isolates. Instead, they showed a one-banded pattern, aligning them with other evolutionarily recent M. ***tuberculosis*** isolates of the PGG2 and PGG3 groups, such as Haarlem, Latin-American and Mediterranean (LAM), and X families. The presence of a nitrate reductase producer phenotype in "Mycobacterium canettii" and some "ancestral" M. ***tuberculosis*** isolates, despite a two-band -215C genotype, argues in favor of an alternate mechanism to explain the differential nitrate reductase activity of certain PGG1 subspecies of the MTC. Overall, these findings may help to establish the precise evolutionary history of important genotype families such as W-Beijing and suggest that the -215T genotype may have contributed the virulence, spread, and evolutionary success of "modern" M. ***tuberculosis*** strains compared to the remaining MTC organisms.

RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Molecular evolutionary history of tubercle bacilli assessed by study of the polymorphic nucleotide within the nitrate reductase (***narGHJI***) operon promoter

AB A well-characterized collection of Mycobacterium ***tuberculosis*** complex (MTC) isolates, representing all known subspecies as well as some relevant genotypic families of M. ***tuberculosis*** , was analyzed for the newly discovered ***narGHJI*** -215 C-to-T promoter single-nucleotide polymorphism (SNP). This point mutation has been shown in earlier studies to be responsible for the differential nitrate reductase activity of M. ***tuberculosis*** vs. M. bovis. As previously defined by the presence or the absence of the TbD1 genetic locus, the group included. . . the "modern" W-Beijing, Haarlem, and Central-Asian1 (CAS1) families as well as the "ancestral" East-African-Indian (EAI) clade. Interestingly, among "modern" M. ***tuberculosis*** isolates, those previously classified as Principal Genetic Group 1 (PGG1) organisms by katG463-gyrA95 polymorphism anal. did not present the two-banded ***narGHJI*** restriction fragment length polymorphism anal. of PCR products pattern common to the other PGG1 MTC members, including the "ancestral" M. ***tuberculosis*** isolates. Instead, they showed a one-banded pattern, aligning them with other evolutionarily recent M. ***tuberculosis*** isolates of the PGG2 and PGG3 groups, such as Haarlem, Latin-American and Mediterranean (LAM), and X families. The presence of a nitrate reductase producer phenotype in "Mycobacterium canettii" and some "ancestral" M. ***tuberculosis*** isolates, despite a two-band -215C genotype, argues in favor of an alternate mechanism to explain the differential nitrate reductase activity. . . as W-Beijing and suggest that the -215T genotype may have contributed the virulence, spread, and evolutionary success of "modern" M. ***tuberculosis*** strains compared to the remaining MTC organisms.

ST operon ***narGHJI*** promoter SNP Mycobacterium phylogeny

IT Mycobacterium ***tuberculosis***
(complex; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Mycobacterium bovis
(mol. evolutionary history of tubercle bacilli assessed by study of

polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Evolution
(mol., mol. phylogeny; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Operon
(***narGHJI*** ; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Promoter (genetic element)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(operon ***narGHJI*** , SNP in; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Genetic polymorphism
(single nucleotide; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT 9013-03-0, Nitrate reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

L7 ANSWER 3 OF 9 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:802885 CAPLUS <<LOGINID::20080825>>
DN 141:290059
TI A single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium ***tuberculosis***
IN Bange, Franz-christoph
PA Artus- Gesellschaft Fuer Molekularbiologische Diagnostik Und Entwicklung Mbh, Germany
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004083459	A1	20040930	WO 2004-EP2911	20040319
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
DE 10313791	A1	20041007	DE 2003-10313791	20030320
AU 2004221678	A1	20040930	AU 2004-221678	20040319
CA 2519702	A1	20040930	CA 2004-2519702	20040319
EP 1606420	A1	20051221	EP 2004-721892	20040319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				

IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK

JP 2006521797 T 20060928 JP 2006-504758 20040319

US 20070015157 A1 20070118 US 2005-549495 20050915

IN 2005DN04651 A 20070817 IN 2005-DN4651 20051013

PRAI DE 2003-10313791 A 20030320

WO 2004-EP2911 W 20040319

AB A single nucleotide polymorphism (SNP) in the ***narGHJI*** operon of Mycobacterium ***tuberculosis*** is used to identify the bacterium in a biol. sample and to differentiate it from other members of the M. ***tuberculosis*** complex.

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI A single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium ***tuberculosis***

AB A single nucleotide polymorphism (SNP) in the ***narGHJI*** operon of Mycobacterium ***tuberculosis*** is used to identify the bacterium in a biol. sample and to differentiate it from other members of the M. ***tuberculosis*** complex.

ST ***tuberculosis*** diagnosis Mycobacterium ***narGHJI*** operon SNP promoter

IT Mycobacterium ***tuberculosis***
Test kits
(SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Animal tissue
(biopsy, detection of Mycobacterium ***tuberculosis*** in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Lung
(bronchial lavage, detection of Mycobacterium ***tuberculosis*** in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Blood
Body fluid
Bone marrow
Cerebrospinal fluid
Feces
Sputum
Stomach content
Urine
Urine analysis
(detection of Mycobacterium ***tuberculosis*** in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Nucleic acid amplification (method)
PCR (polymerase chain reaction)
(for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Primers (nucleic acid)
Probes (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT ***Tuberculosis***

(mol. diagnosis of; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Diagnosis
(mol.; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Promoter (genetic element)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***narGHJI*** operon; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Operon
(***narGHJI*** , promoter of; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT DNA sequences
(of promoter of ***narGHJI*** operon of Mycobacterium ***tuberculosis*** ; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT PCR (polymerase chain reaction)
(real-time, for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT Genetic polymorphism
(single nucleotide; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT 9013-03-0, Nitrate reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***narGHJI*** operon for; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT 765198-22-9
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT 765198-17-2 765198-18-3 765198-19-4 765198-20-7 765198-21-8
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium ***tuberculosis***)

IT 765198-46-7 765198-47-8
RL: PRP (Properties)
(unclaimed sequence; single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium ***tuberculosis***)

L7 ANSWER 4 OF 9 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 3
AN 2004:848168 CAPLUS <<LOGINID::20080825>>
DN 142:71384
TI The species Mycobacterium africanum in the light of new molecular markers
AU Niemann, S.; Kubica, T.; Bange, F. C.; Adjei, O.; Browne, E. N.; Chinbuah, M. A.; Diel, R.; Gyapong, J.; Horstmann, R. D.; Joloba, M. L.; Meyer, C. G.; Mugerwa, R. D.; Okwera, A.; Osei, I.; Owusu-Darbo, E.; Schwander, S. K.; Ruesch-Gerdes, S.
CS National Reference Center for Mycobacteria, Forschungszentrum Borstel, Borstel, Germany

SO Journal of Clinical Microbiology (2004), 42(9), 3958-3962
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB The findings of recent studies addressing the mol. characteristics of Mycobacterium ***tuberculosis*** complex isolates have initiated a discussion on the classification of M. africanum, esp. of those isolates originating from East Africa (cluster F, subtype II) and displaying phenotypic and biochem. characteristics more similar to those of M. ***tuberculosis*** . To further address this question, the authors analyzed a representative collection of 63 M. ***tuberculosis*** complex strains comprising 30 M. africanum subtype I strains, 20 M. africanum subtype II strains, 10 randomly chosen M. ***tuberculosis*** isolates, and type strains of M. ***tuberculosis*** , M. bovis, and M. africanum for the following biochem. and mol. characteristics: single-nucleotide polymorphisms (SNPs) in gyrB and ***narGHJI*** and the presence or absence of RD1, RD9, and RD12. For all mol. markers analyzed, subtype II strains were identical to the M. ***tuberculosis*** strains tested. In contrast, the subtype I strains as well as the M. africanum type strain showed unique combinations of SNPs in gyrB and genomic deletions (the absence of RD9 and the presence of RD12), which proves their independence from M. ***tuberculosis*** and M. bovis. Accordingly, all subtype I strains displayed main biochem. characteristics included in the original species description of M. africanum. We conclude that the isolates from West Africa were proved to be M. africanum with respect to the phenotypic and genetic markers analyzed, while the isolates from East Africa must be regarded as phenotypic variants of M. ***tuberculosis*** (genotype Uganda). We propose the addn. of the mol. characteristics defined here to the species description of M. africanum, which will allow clearer species differentiation in the future.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB The findings of recent studies addressing the mol. characteristics of Mycobacterium ***tuberculosis*** complex isolates have initiated a discussion on the classification of M. africanum, esp. of those isolates originating from East Africa (cluster F, subtype II) and displaying phenotypic and biochem. characteristics more similar to those of M. ***tuberculosis*** . To further address this question, the authors analyzed a representative collection of 63 M. ***tuberculosis*** complex strains comprising 30 M. africanum subtype I strains, 20 M. africanum subtype II strains, 10 randomly chosen M. ***tuberculosis*** isolates, and type strains of M. ***tuberculosis*** , M. bovis, and M. africanum for the following biochem. and mol. characteristics: single-nucleotide polymorphisms (SNPs) in gyrB and ***narGHJI*** and the presence or absence of RD1, RD9, and RD12. For all mol. markers analyzed, subtype II strains were identical to the M. ***tuberculosis*** strains tested. In contrast, the subtype I strains as well as the M. africanum type strain showed unique combinations of. . . in gyrB and genomic deletions (the absence of RD9 and the presence of RD12), which proves their independence from M. ***tuberculosis*** and M. bovis. Accordingly, all subtype I strains displayed main biochem. characteristics included in the original species description of M.. . . the phenotypic and genetic markers analyzed, while the isolates from East Africa must be regarded as phenotypic variants of M. ***tuberculosis*** (genotype Uganda). We propose the addn. of the mol. characteristics defined here to the species description of M. africanum, which. . .

ST genetic polymorphism biomarker genotype gyrB ***narGHJI*** Mycobacterium
IT Promoter (genetic element)
RL: BSU (Biological study, unclassified); BIOL (Biological study) (early, ***narGHJI*** ; mol. markers of Mycobacterium africanum)

L7 ANSWER 5 OF 9 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 4
AN 2004:305778 BIOSIS <<LOGINID::20080825>>
DN PREV200400304326
TI A promoter mutation causes differential nitrate reductase activity of Mycobacterium ***tuberculosis*** and Mycobacterium bovis.
AU Stermann, Marion; Sedlacek, Ludwig; Maass, Silvia; Bange, Franz-Christoph [Reprint Author]
CS Dept Med Microbiol and Hosp Epidemiol, Hannover Med Sch, Carl Neuberg Str 1, D-30625, Hanover, Germany
bange@mikrobio.mh-hannover.de
SO Journal of Bacteriology, (May 2004) Vol. 186, No. 9, pp. 2856-2861. print. CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 7 Jul 2004
Last Updated on STN: 7 Jul 2004
AB The recent publication of the genome sequence of Mycobacterium bovis showed >99.95% identity to M. ***tuberculosis*** . No genes unique to M. bovis were found. Instead numerous single-nucleotide polymorphisms (SNPs) were identified. This has led to the hypothesis that differential gene expression due to SNPs might explain the differences between the human and bovine tubercle bacilli. One phenotypic distinction between M. ***tuberculosis*** and M. bovis is nitrate reduction, which not only is an essential diagnostic tool but also contributes to mycobacterial pathogenesis. We previously showed that ***narGHJI*** encodes a nitrate reductase in both M. ***tuberculosis*** and M. bovis and that ***NarGHJI*** -mediated nitrate reductase activity was substantially higher in the human tubercle bacillus. In the present study we used a genetic approach to demonstrate that an SNP within the promoter of the nitrate reductase gene cluster ***narGHJI*** is responsible for the different nitrate reductase activity of M. ***tuberculosis*** and M. bovis. This is the first example of an SNP that leads to differential gene expression between the human and bovine tubercle bacilli.
TI A promoter mutation causes differential nitrate reductase activity of Mycobacterium ***tuberculosis*** and Mycobacterium bovis.
AB The recent publication of the genome sequence of Mycobacterium bovis showed >99.95% identity to M. ***tuberculosis*** . No genes unique to M. bovis were found. Instead numerous single-nucleotide polymorphisms (SNPs) were identified. This has led to the. . . expression due to SNPs might explain the differences between the human and bovine tubercle bacilli. One phenotypic distinction between M. ***tuberculosis*** and M. bovis is nitrate reduction, which not only is an essential diagnostic tool but also contributes to mycobacterial pathogenesis. We previously showed that ***narGHJI*** encodes a nitrate reductase in both M. ***tuberculosis*** and M. bovis and that ***NarGHJI*** -mediated nitrate reductase activity was substantially higher in the human tubercle bacillus. In the present study we used a genetic approach to demonstrate that an SNP within the promoter of the nitrate reductase gene cluster ***narGHJI*** is responsible for the different nitrate reductase activity of M. ***tuberculosis*** and M. bovis. This is the first

example of an SNP that leads to differential gene expression between the human. . .

ORGN . . .
Mycobacteriaceae 08881
Super Taxa
Mycobacteria; Actinomycetes and Related Organisms; Eubacteria;
Bacteria; Microorganisms
Organism Name
Mycobacterium bovis (species): pathogen
Mycobacterium spp. (species)
Mycobacterium ***tuberculosis*** (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L7 ANSWER 6 OF 9 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 5
AN 2004:31083 BIOSIS <<LOGINID::20080825>>
DN PREV200400023668
TI Role of narK2X and ***narGHJI*** in hypoxic upregulation of nitrate reduction by Mycobacterium ***tuberculosis*** .
AU Sohaskey, Charles D. [Reprint Author]; Wayne, Lawrence G.
CS Tuberculosis Research Laboratory (151), Department of Veterans Affairs Medical Center, 5901 East Seventh St., Long Beach, CA, 90822, USA
chuck@sohaskey.com
SO Journal of Bacteriology, (December 2003) Vol. 185, No. 24, pp. 7247-7256. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 31 Dec 2003
Last Updated on STN: 31 Dec 2003
AB Mycobacterium ***tuberculosis*** is one of the strongest reducers of nitrate in the genus Mycobacterium. Under microaerobic conditions, whole cells exhibit upregulation of activity, producing approximately eightfold more nitrite than those of aerobic cultures of the same age. Assays of cell extracts from aerobic cultures and hypoxic cultures yielded comparable nitrate reductase activities. Mycobacterium bovis produced only low levels of nitrite, and this activity was not induced by hypoxia. M. ***tuberculosis*** has two sets of genes, ***narGHJI*** and narX of the narK2X operon, that exhibit some degree of homology to prokaryotic dissimilatory nitrate reductases. Each of these were knocked out by insertional inactivation. The narG mutant showed no nitrate reductase activity in whole culture or in cell-free assays, while the narX mutant showed wild-type levels in both assays. A knockout of the putative nitrite transporter narK2 gene produced a strain that had aerobic levels of nitrate reductase activity but failed to show hypoxic upregulation. Insertion of the M. ***tuberculosis*** ***narGHJI*** into a nitrate reductase Escherichia coli mutant allowed anaerobic growth in the presence of nitrate. Under aerobic and hypoxic conditions, transcription of ***narGHJI*** was constitutive, while the narK2X operon was induced under hypoxia, as measured with a lacZ reporter system and by quantitative real-time reverse PCR. This indicates that nitrate reductase activity in M. ***tuberculosis*** is due to the ***narGHJI*** locus with no detectable contribution from narX and that the hypoxic upregulation of activity is associated with the induction of the nitrate and nitrite transport gene narK2.
TI Role of narK2X and ***narGHJI*** in hypoxic upregulation of nitrate

reduction by Mycobacterium ***tuberculosis*** .

AB Mycobacterium ***tuberculosis*** is one of the strongest reducers of nitrate in the genus Mycobacterium. Under microaerobic conditions, whole cells exhibit upregulation of. . . nitrate reductase activities. Mycobacterium bovis produced only low levels of nitrite, and this activity was not induced by hypoxia. M. ***tuberculosis*** has two sets of genes, ***narGHJI*** and narX of the narK2X operon, that exhibit some degree of homology to prokaryotic dissimilatory nitrate reductases. Each of these. . . a strain that had aerobic levels of nitrate reductase activity but failed to show hypoxic upregulation. Insertion of the M. ***tuberculosis*** ***narGHJI*** into a nitrate reductase Escherichia coli mutant allowed anaerobic growth in the presence of nitrate. Under aerobic and hypoxic conditions, transcription of ***narGHJI*** was constitutive, while the narK2X operon was induced under hypoxia, as measured with a lacZ reporter system and by quantitative real-time reverse PCR. This indicates that nitrate reductase activity in M. ***tuberculosis*** is due to the ***narGHJI*** locus with no detectable contribution from narX and that the hypoxic upregulation of activity is associated with the induction of. . .

ORGN Classifier
Mycobacteriaceae 08881
Super Taxa
Mycobacteria; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms
Organism Name
Mycobacterium bovis (species)
Mycobacterium ***tuberculosis*** (species)
Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN Mycobacterium ***tuberculosis*** ***narGHJI*** gene (Mycobacteriaceae); Mycobacterium ***tuberculosis*** narK2 gene (Mycobacteriaceae); Mycobacterium ***tuberculosis*** narK2X gene (Mycobacteriaceae); Mycobacterium ***tuberculosis*** narX gene (Mycobacteriaceae)

L7 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 6
AN 2003:641546 CAPLUS <<LOGINID::20080825>>
DN 139:302761
TI Polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***
AU Stermann, Marion; Bohrssen, Antje; Diephaus, Catharina; Maass, Silvia; Bange, Franz-Christoph
CS Department of Medical Microbiology and Hospital Epidemiology, Medical School Hannover, Hannover, 30625, Germany
SO Journal of Clinical Microbiology (2003), 41(7), 3252-3259
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English

AB Mycobacterium ***tuberculosis*** rapidly reduces nitrate, leading to the accumulation of nitrite. This characteristic served for the past 40 yr to differentiate M. ***tuberculosis*** from other members of the Mycobacterium ***tuberculosis*** complex (MTBC), such as Mycobacterium bovis (non-BCG [referred to here as simply "M. bovis"]), Mycobacterium bovis BCG, Mycobacterium africanum, or Mycobacterium microti. Here, a narG deletion in M. ***tuberculosis*** showed that rapid nitrite accumulation of M. ***tuberculosis*** is mediated by ***narGHJI***

. Anal. of narG mutants of M. bovis and M. bovis BCG showed that, as in M. ***tuberculosis*** , nitrite accumulation was mediated by ***narGHJI*** , and no other nitrate reductase was involved. However, in contrast to M. ***tuberculosis*** , accumulation was delayed for several days. Comparison of the ***narGHJI*** promoter revealed that, at nucleotide -215 prior to the start codon of narG, M. ***tuberculosis*** carried a thymine residue, whereas the bovine mycobacteria carried a cytosine residue. Using LightCycler technol. we examd. 62 strains of M. ***tuberculosis*** , M. bovis, M. bovis BCG, M. microti, and M. africanum and demonstrated that this single nucleotide polymorphism was specific for M. ***tuberculosis*** . For further differentiation within the MTBC, we included, by using LightCycler technol., the previously described anal. of oxyR polymorphism, which is specific for the bovine mycobacteria, and the RD1 polymorphism, which is specific for M. bovis BCG. Based on these results, we suggest a LightCycler format for rapid and unambiguous diagnosis of M. ***tuberculosis*** , M. bovis, and M. bovis BCG.

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***

AB Mycobacterium ***tuberculosis*** rapidly reduces nitrate, leading to the accumulation of nitrite. This characteristic served for the past 40 yr to differentiate M. ***tuberculosis*** from other members of the Mycobacterium ***tuberculosis*** complex (MTBC), such as Mycobacterium bovis (non-BCG [referred to here as simply "M. bovis"]), Mycobacterium bovis BCG, Mycobacterium africanum, or Mycobacterium microti. Here, a narG deletion in M. ***tuberculosis*** showed that rapid nitrite accumulation of M. ***tuberculosis*** is mediated by ***narGHJI*** . Anal. of narG mutants of M. bovis and M. bovis BCG showed that, as in M. ***tuberculosis*** , nitrite accumulation was mediated by ***narGHJI*** , and no other nitrate reductase was involved. However, in contrast to M. ***tuberculosis*** , accumulation was delayed for several days. Comparison of the ***narGHJI*** promoter revealed that, at nucleotide -215 prior to the start codon of narG, M. ***tuberculosis*** carried a thymine residue, whereas the bovine mycobacteria carried a cytosine residue. Using LightCycler technol. we examd. 62 strains of M. ***tuberculosis*** , M. bovis, M. bovis BCG, M. microti, and M. africanum and demonstrated that this single nucleotide polymorphism was specific for M. ***tuberculosis*** . For further differentiation within the MTBC, we included, by using LightCycler technol., the previously described anal. of oxyR polymorphism, which. . . for M. bovis BCG. Based on these results, we suggest a LightCycler format for rapid and unambiguous diagnosis of M. ***tuberculosis*** , M. bovis, and M. bovis BCG.

ST Mycobacterium nitrate reductase ***narGHJI*** promoter polymorphism

IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(narG; polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)

IT Operon
(***narGHJI*** ; polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)

IT Promoter (genetic element)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***narGHJI*** ; polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(oxyR; polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)
IT Genetic polymorphism
Mycobacterium africanum
Mycobacterium bovis
Mycobacterium microti
Mycobacterium ***tuberculosis***
(polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)
IT 9013-03-0, Nitrate reductase 14797-65-0, Nitrite, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(polymorphic nucleotide within the promoter of nitrate reductase (***NarGHJI***) is specific for Mycobacterium ***tuberculosis***)

L7 ANSWER 8 OF 9 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 7
AN 2002:144790 BIOSIS <<LOGINID::20080825>>
DN PREV200200144790
TI Dependence of Mycobacterium bovis BCG on anaerobic nitrate reductase for persistence is tissue specific.
AU Fritz, Christian; Maass, Silvia; Kreft, Andreas; Bange, Franz-Christoph [Reprint author]
CS Institute fuer Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany
bange@mikrobio.mh-hannover.de
SO Infection and Immunity, (January, 2002) Vol. 70, No. 1, pp. 286-291. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 14 Feb 2002
Last Updated on STN: 26 Feb 2002
AB Mycobacterium bovis BCG, the only presently available vaccine against ***tuberculosis*** , was obtained from virulent M. bovis after serial passages in vitro. The vaccine strain retained at least some of its original virulence, as it persists in immune-competent hosts and occasionally may cause fatal disease in immune-deficient hosts. Mycobacterial persistence in vivo is thought to depend on anaerobic metabolism, an apparent paradox since all mycobacteria are obligate aerobes. Here we report that M. bovis BCG lacking anaerobic nitrate reductase (***NarGHJI***), an enzyme essential for nitrate respiration, failed to persist in the lungs, liver, and kidneys of immune-competent (BALB/c) mice. In immune-deficient (SCID) mice, however, bacilli caused chronic infection despite disruption of narG, even if growth of the mutant was severely impaired in lungs, liver, and kidneys. Persistence and growth of BCG in the spleens of either mouse strain appeared largely unaffected by lack of anaerobic nitrate reductase, indicating that the role of the enzyme in pathogenesis is tissue specific. These data suggest first that anaerobic nitrate reduction is essential for

metabolism of M. bovis BCG in immune-competent but not immune-deficient mice and second that its role in mycobacterial disease is tissue specific, both of which are observations with important implications for pathogenesis of mycobacteria and vaccine development.

AB Mycobacterium bovis BCG, the only presently available vaccine against ***tuberculosis*** , was obtained from virulent M. bovis after serial passages in vitro. The vaccine strain retained at least some of its. . . an apparent paradox since all mycobacteria are obligate aerobes. Here we report that M. bovis BCG lacking anaerobic nitrate reductase (***NarGHJI***), an enzyme essential for nitrate respiration, failed to persist in the lungs, liver, and kidneys of immune-competent (BALB/c) mice. In. . .

L7 ANSWER 9 OF 9 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 8

AN 2000:182005 BIOSIS <<LOGINID::20080825>>

DN PREV200000182005

TI Anaerobic nitrate reductase (***narGHJI***) activity of Mycobacterium bovis BCG in vitro and its contribution to virulence in immunodeficient mice.

AU Weber, Isabel; Fritz, Christian; Ruttkowski, Silvia; Kreft, Andreas; Bange, Franz-Christoph [Reprint author]

CS Institute of Medical Microbiology, Medical School Hannover, Carl-Neuberg-Strasse 1, 30625, Hannover, Germany

SO Molecular Microbiology, (March, 2000) Vol. 35, No. 5, pp. 1017-1025. print.
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 11 May 2000
Last Updated on STN: 4 Jan 2002

AB Mycobacterium ***tuberculosis*** and Mycobacterium bovis cause ***tuberculosis*** , which is responsible for the deaths of more people each year than any other bacterial infectious disease. Disseminated disease with Mycobacterium bovis BCG, the only currently available vaccine against ***tuberculosis*** , occurs in immunocompetent and immunodeficient individuals. Although mycobacteria are obligate aerobes, they are thought to face an anaerobic environment during infection, notably inside abscesses and granulomas. The purpose of this study was to define a metabolic pathway that could allow mycobacteria to exist under these conditions. Recently, the complete genome of M. ***tuberculosis*** has been sequenced, and genes homologous to an anaerobic nitrate reductase (***narGHJI***), an enzyme allowing nitrate respiration when oxygen is absent, were found. Here, we show that the ***narGHJI*** cluster of M. ***tuberculosis*** is functional as it conferred anaerobic nitrate reductase activity to Mycobacterium smegmatis. A narG mutant of M. bovis BCG was generated by targeted gene deletion. The mutant lacked the ability to reduce nitrate under anaerobic conditions. Both mutant and M. bovis BCG wild type grew equally well under aerobic conditions in vitro. Histology of immunodeficient mice (SCID) infected with M. bovis BCG wild type revealed large granulomas teeming with acid-fast bacilli; all mice showed signs of clinical disease after 50 days and succumbed after 80 days. In contrast, mice infected with the mutant had smaller granulomas containing fewer bacteria; these mice showed no signs of clinical disease after more than 200 days. Thus, it seems that nitrate respiration contributes significantly to virulence of M. bovis BCG in immunodeficient SCID mice.

TI Anaerobic nitrate reductase (***narGHJI***) activity of Mycobacterium bovis BCG in vitro and its contribution to virulence in immunodeficient mice.

AB Mycobacterium ***tuberculosis*** and Mycobacterium bovis cause ***tuberculosis*** , which is responsible for the deaths of more people each year than any other bacterial infectious disease. Disseminated disease with Mycobacterium bovis BCG, the only currently available vaccine against ***tuberculosis*** , occurs in immunocompetent and immunodeficient individuals. Although mycobacteria are obligate aerobes, they are thought to face an anaerobic environment during. . . to define a metabolic pathway that could allow mycobacteria to exist under these conditions. Recently, the complete genome of M. ***tuberculosis*** has been sequenced, and genes homologous to an anaerobic nitrate reductase (***narGHJI***), an enzyme allowing nitrate respiration when oxygen is absent, were found. Here, we show that the ***narGHJI*** cluster of M. ***tuberculosis*** is functional as it conferred anaerobic nitrate reductase activity to Mycobacterium smegmatis. A narG mutant of M. bovis BCG was. . .

IT Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Immune System (Chemical Coordination and Homeostasis); Infection

IT Diseases
tuberculosis : bacterial disease
Tuberculosis (MeSH)

IT Chemicals & Biochemicals
anaerobic nitrate reductase: activities, analysis, functions; enzymes; vaccines

ORGN . . .

ORGN Classifier
Mycobacteriaceae 08881

Super Taxa
Mycobacteria; Actinomycetes and Related Organisms; Eubacteria; Bacteria; Microorganisms

Organism Name
Mycobacterium bovis: BCG, pathogen
Mycobacterium ***tuberculosis*** : pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

=> s PCR and narGHJI
L8 24 PCR AND NARGHJI

=> dup rem l8
PROCESSING COMPLETED FOR L8
L9 10 DUP REM L8 (14 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 10 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 2008:193416 BIOSIS <<LOGINID::20080825>>
DN PREV200800189257
TI Anaerobic growth of Corynebacterium glutamicum using nitrate as a terminal electron acceptor.
AU Nishimura, T. [Reprint Author]; Vertes, A. A.; Shinoda, Y.; Inui, M.; Yukawa, H.

CS Res Inst Innovat Technol Earth, Kyoto, Japan
SO Abstracts of the General Meeting of the American Society for Microbiology, (2007) Vol. 107, pp. 344.
Meeting Info.: 107th General Meeting of the American-Society-for-Microbiology. Toronto, CANADA. 2007,. Amer Soc Microbiol.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; (Meeting Poster)
LA English
ED Entered STN: 19 Mar 2008
Last Updated on STN: 19 Mar 2008
IT Methods & Equipment
RT- ***PCR*** [reverse transcriptase-polymerase chain reaction]: laboratory techniques, genetic techniques; primer extension analysis: laboratory techniques, genetic techniques
IT Miscellaneous Descriptors
anaerobic respiration;. . .
GEN Escherichia coli narK gene (Enterobacteriaceae); Corynebacterium glutamicum narKGHJI gene (Irregular Nonsporing Gram-Positive Rods); Escherichia coli ***narGHJI*** gene (Enterobacteriaceae); Corynebacterium glutamicum narG gene (Irregular Nonsporing Gram-Positive Rods): mutant; Corynebacterium glutamicum narH gene (Irregular Nonsporing Gram-Positive Rods): mutant

L9 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2006:1043204 CAPLUS <<LOGINID::20080825>>
DN 146:1456
TI Whole-genome transcriptional analysis of chemolithoautotrophic thiosulfate oxidation by Thiobacillus denitrificans under aerobic versus denitrifying conditions
AU Beller, Harry R.; Letain, Tracy E.; Chakicherla, Anu; Kane, Staci R.; Legler, Tina C.; Coleman, Matthew A.
CS Lawrence Livermore National Laboratory, Livermore, CA, 94551, USA
SO Journal of Bacteriology (2006), 188(19), 7005-7015
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Thiobacillus denitrificans is one of the few known obligate chemolithoautotrophic bacteria capable of energetically coupling thiosulfate oxidn. to denitrification as well as aerobic respiration. As very little is known about the differential expression of genes assocd. with key chemolithoautotrophic functions (such as sulfur compd. oxidn. and CO2 fixation) under aerobic vs. denitrifying conditions, we conducted whole-genome, cDNA microarray studies to explore this topic systematically. The microarrays identified 277 genes (approx. 10% of the genome) as differentially expressed using RMA (robust multiarray av.) statistical anal. and a twofold cutoff. Genes upregulated (.apprx.6- to 150-fold) under aerobic conditions included a cluster of genes assocd. with iron acquisition (e.g., siderophore-related genes), a cluster of cytochrome cbb3 oxidase genes, cbbL and cbbS (encoding the large and small subunits of form I ribulose 1,5-bisphosphate carboxylase/oxygenase, or RubisCO), and multiple mol. chaperone genes. Genes upregulated (.apprx.4- to 95-fold) under denitrifying conditions included nar, nir, and nor genes (assocd., resp., with nitrate reductase, nitrite reductase, and nitric oxide reductase, which catalyze successive steps of denitrification), cbbM (encoding form II RubisCO), and genes involved with sulfur compd. oxidn.

(including two phys. sepd. but highly similar copies of sulfide:quinone oxidoreductase and of dsrC, assocd. with dissimilatory sulfite reductase). Among genes assocd. with denitrification, relative expression levels (i.e., degree of upregulation with nitrate) tended to decrease in the order nar > nir > nor > nos. Reverse transcription-quant. ***PCR*** anal. was used to validate these trends.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB . . . degree of upregulation with nitrate) tended to decrease in the order nar > nir > nor > nos. Reverse transcription-quant. ***PCR*** anal. was used to validate these trends.

IT Operon
(***narGHJI*** , upregulated under denitrifying conditions; whole-genome transcriptional anal. of chemolithoautotrophic thiosulfate oxidn. by Thiobacillus denitrificans under aerobic vs. denitrifying conditions)

L9 ANSWER 3 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 1

AN 2006:572874 BIOSIS <<LOGINID::20080825>>

DN PREV200600579306

TI Role of the Escherichia coli nitrate transport protein, NarU, in survival during severe nutrient starvation and slow growth.

AU Clegg, Stephanie J.; Jia, Wenjing; Cole, Jeffrey A. [Reprint Author]

CS Univ Birmingham, Sch Biosci, Birmingham B15 2TT, W Midlands, UK
j.a.cole@bham.ac.uk

SO Microbiology (Reading), (JUL 2006) Vol. 152, No. Part 7, pp. 2091-2100.
ISSN: 1350-0872.

DT Article

LA English

ED Entered STN: 1 Nov 2006
Last Updated on STN: 1 Nov 2006

AB Escherichia coli K-12 strains expressing either NarU or NarK as the only nitrate transport protein are both able to support nitrate-dependent anaerobic growth. The narK gene is highly expressed during anaerobic growth in the presence of nitrate, consistent with a role for NarK in nitrate transport coupled to nitrate reduction by the most active nitrate reductase encoded by the adjacent ***narGHJI*** operon. The physiological role of NarU is unknown. Reverse transcriptase ***PCR*** experiments established that, unlike the monocistronic narK gene, narU is co-transcribed with narZ as the first gene of a five-gene narUZYWV operon. The narK and narU genes were fused in-frame to a myc tag: the encoded fusion proteins complemented the nitrate-dependent growth defect of chromosomal narK and narU mutations. A commercial anti-Myc antibody was used to detect NarK and NarU in membrane fractions. During anaerobic growth in the presence of nitrate, the quantity of NarU-Myc accumulated during exponential growth was far less than that of NarK-Myc, but NarU was more abundant than NarK in stationary-phase cultures in the absence of nitrate. Although the concentration of NarU-Myc increased considerably during the post-exponential phase of growth, NarK-Myc was still more abundant than NarU-Myc in stationary-phase bacteria in the presence of nitrate, In chemostat competition experiments, a strain expressing only narU had a selective advantage relative to a strain expressing only narK during nutrient starvation or very slow growth, but NarK(+) bacteria had a much greater selective advantage during rapid growth. The data suggest that NarU confers a selective advantage during severe nutrient starvation or slow growth, conditions similar to those encountered in vivo.

AB. . . role for NarK in nitrate transport coupled to nitrate reduction by the most active nitrate reductase encoded by the adjacent ***narGHJI*** operon. The physiological role of NarU is unknown. Reverse transcriptase ***PCR*** experiments established that, unlike the monocistronic narK gene, narU is co-transcribed with narZ as the first gene of a five-gene. . .

L9 ANSWER 4 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 2
AN 2007:110931 BIOSIS <<LOGINID::20080825>>
DN PREV200700113067
TI A membrane-bound nitrate reductase encoded by the ***narGHJI*** operon is responsible for anaerobic respiration in Halomonas maura.
AU Argandona, Montserrat; Martinez-Checa, Fernando; Llamas, Inmaculada; Arco, Yolanda; Quesada, Emilia; del Moral, Ana [Reprint Author]
CS Univ Granada, Dept Microbiol, Fac Pharm, Campus Univ Cartuja S-N, Granada 18071, Spain
admoral@ugr.es
SO Extremophiles, (OCT 2006) Vol. 10, No. 5, pp. 411-419.
ISSN: 1431-0651.
DT Article
LA English
ED Entered STN: 14 Feb 2007
Last Updated on STN: 14 Feb 2007
AB The halophilic bacterium Halomonas maura is capable of anaerobic respiration on nitrates. By insertional mutagenesis with the minitransposon Tn-5 we obtained the mutant Tc62, which was incapable of anaerobic respiration on nitrates. An analysis of the regions adjacent to the transposon allowed us to characterize the membrane-bound anaerobic-respiratory nitrate reductase ***narGHJI*** gene cluster in H. maura. We identified consensus sequences for fumarate and nitrate reductase regulator (FNR)-like protein-binding sites in the promoter regions of the nar genes and consensus sequences corresponding to the NarL binding sites upstream of the nar genes. RT- ***PCR*** analysis showed that the ***narGHJI*** operon was expressed in response to anaerobic conditions when nitrate was available as electron acceptor. This membrane-bound nitrate reductase is the only enzyme responsible for anaerobic respiration on nitrate in H. maura. In this article we discuss the possible relationship between this enzyme and a dissimilatory nitrate-reduction-to-ammonia process (DNRA) in H. maura and its role in the colonization of the rhizosphere.
TI A membrane-bound nitrate reductase encoded by the ***narGHJI*** operon is responsible for anaerobic respiration in Halomonas maura.
AB. . . on nitrates. An analysis of the regions adjacent to the transposon allowed us to characterize the membrane-bound anaerobic-respiratory nitrate reductase ***narGHJI*** gene cluster in H. maura. We identified consensus sequences for fumarate and nitrate reductase regulator (FNR)-like protein-binding sites in the. . . promoter regions of the nar genes and consensus sequences corresponding to the NarL binding sites upstream of the nar genes. RT- ***PCR*** analysis showed that the ***narGHJI*** operon was expressed in response to anaerobic conditions when nitrate was available as electron acceptor. This membrane-bound nitrate reductase is. . .

L9 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 3
AN 2005:984897 CAPLUS <<LOGINID::20080825>>
DN 144:289142

TI Molecular evolutionary history of tubercle bacilli assessed by study of the polymorphic nucleotide within the nitrate reductase (***narGHJI***) operon promoter

AU Goh, Khye Seng; Rastogi, Nalin; Berchel, Mylene; Huard, Richard C.; Sola, Christophe

CS Unite de la Tuberculose et des Mycobacteries, Institut Pasteur de Guadeloupe, Pointe-a-Pitre, Guam

SO Journal of Clinical Microbiology (2005), 43(8), 4010-4014
CODEN: JCMIDW; ISSN: 0095-1137

PB American Society for Microbiology

DT Journal

LA English

AB A well-characterized collection of Mycobacterium tuberculosis complex (MTC) isolates, representing all known subspecies as well as some relevant genotypic families of M. tuberculosis, was analyzed for the newly discovered ***narGHJI*** -215 C-to-T promoter single-nucleotide polymorphism (SNP). This point mutation has been shown in earlier studies to be responsible for the differential nitrate reductase activity of M. tuberculosis vs. M. bovis. As previously defined by the presence or the absence of the TbD1 genetic locus, the group included both the "modern" W-Beijing, Haarlem, and Central-Asian1 (CAS1) families as well as the "ancestral" East-African-Indian (EAI) clade. Interestingly, among "modern" M. tuberculosis isolates, those previously classified as Principal Genetic Group 1 (PGG1) organisms by katG463-gyrA95 polymorphism anal. did not present the two-banded ***narGHJI*** restriction fragment length polymorphism anal. of ***PCR*** products pattern common to the other PGG1 MTC members, including the "ancestral" M. tuberculosis isolates. Instead, they showed a one-banded pattern, aligning them with other evolutionarily recent M. tuberculosis isolates of the PGG2 and PGG3 groups, such as Haarlem, Latin-American and Mediterranean (LAM), and X families. The presence of a nitrate reductase producer phenotype in "Mycobacterium canettii" and some "ancestral" M. tuberculosis isolates, despite a two-band -215C genotype, argues in favor of an alternate mechanism to explain the differential nitrate reductase activity of certain PGG1 subspecies of the MTC. Overall, these findings may help to establish the precise evolutionary history of important genotype families such as W-Beijing and suggest that the -215T genotype may have contributed the virulence, spread, and evolutionary success of "modern" M. tuberculosis strains compared to the remaining MTC organisms.

RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Molecular evolutionary history of tubercle bacilli assessed by study of the polymorphic nucleotide within the nitrate reductase (***narGHJI***) operon promoter

AB . . . representing all known subspecies as well as some relevant genotypic families of M. tuberculosis, was analyzed for the newly discovered ***narGHJI*** -215 C-to-T promoter single-nucleotide polymorphism (SNP). This point mutation has been shown in earlier studies to be responsible for the. . . isolates, those previously classified as Principal Genetic Group 1 (PGG1) organisms by katG463-gyrA95 polymorphism anal. did not present the two-banded ***narGHJI*** restriction fragment length polymorphism anal. of ***PCR*** products pattern common to the other PGG1 MTC members, including the "ancestral" M. tuberculosis isolates. Instead, they showed a one-banded. . .

ST operon ***narGHJI*** promoter SNP Mycobacterium phylogeny

IT Mycobacterium tuberculosis
(complex; mol. evolutionary history of tubercle bacilli assessed by

study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Mycobacterium bovis
(mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Evolution
(mol., mol. phylogeny; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Operon
(***narGHJI*** ; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Promoter (genetic element)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(operon ***narGHJI*** , SNP in; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT Genetic polymorphism
(single nucleotide; mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

IT 9013-03-0, Nitrate reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(mol. evolutionary history of tubercle bacilli assessed by study of polymorphic nucleotide within nitrate reductase (***narGHJI***) operon promoter)

L9 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:802885 CAPLUS <<LOGINID::20080825>>
DN 141:290059
TI A single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium tuberculosis
IN Bange, Franz-christoph
PA Artus- Gesellschaft Fuer Molekularbiologische Diagnostik Und Entwicklung Mbh, Germany
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004083459	A1	20040930	WO 2004-EP2911	20040319
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
DE 10313791	A1	20041007	DE 2003-10313791	20030320

AU 2004221678 A1 20040930 AU 2004-221678 20040319
CA 2519702 A1 20040930 CA 2004-2519702 20040319
EP 1606420 A1 20051221 EP 2004-721892 20040319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK
JP 2006521797 T 20060928 JP 2006-504758 20040319
US 20070015157 A1 20070118 US 2005-549495 20050915
IN 2005DN04651 A 20070817 IN 2005-DN4651 20051013
PRAI DE 2003-10313791 A 20030320
WO 2004-EP2911 W 20040319
AB A single nucleotide polymorphism (SNP) in the ***narGHJI*** operon of Mycobacterium tuberculosis is used to identify the bacterium in a biol. sample and to differentiate it from other members of the M. tuberculosis complex.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI A single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium tuberculosis
AB A single nucleotide polymorphism (SNP) in the ***narGHJI*** operon of Mycobacterium tuberculosis is used to identify the bacterium in a biol. sample and to differentiate it from other. . .
ST tuberculosis diagnosis Mycobacterium ***narGHJI*** operon SNP promoter
IT Mycobacterium tuberculosis
Test kits
(SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Animal tissue
(biopsy, detection of Mycobacterium tuberculosis in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Lung
(bronchial lavage, detection of Mycobacterium tuberculosis in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Blood
Body fluid
Bone marrow
Cerebrospinal fluid
Feces
Sputum
Stomach content
Urine
Urine analysis
(detection of Mycobacterium tuberculosis in; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Nucleic acid amplification (method)
PCR (polymerase chain reaction)
(for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Primers (nucleic acid)
Probes (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of

Mycobacterium tuberculosis)
IT Tuberculosis
(mol. diagnosis of; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Diagnosis
(mol.; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Promoter (genetic element)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***narGHJI*** operon; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Operon
(***narGHJI*** , promoter of; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT DNA sequences
(of promoter of ***narGHJI*** operon of Mycobacterium tuberculosis; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT ***PCR*** (polymerase chain reaction)
(real-time, for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT Genetic polymorphism
(single nucleotide; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT 9013-03-0, Nitrate reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(***narGHJI*** operon for; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT 765198-22-9
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT 765198-17-2 765198-18-3 765198-19-4 765198-20-7 765198-21-8
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(probe for detection of polymorphism in ***narGHJI*** promoter; SNP in ***narGHJI*** promoter for detection and identification of Mycobacterium tuberculosis)
IT 765198-46-7 765198-47-8
RL: PRP (Properties)
(unclaimed sequence; single nucleotide polymorphism in the ***narGHJI*** promoter for the detection and identification of Mycobacterium tuberculosis)

L9 ANSWER 7 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 4
AN 2004:31083 BIOSIS <<LOGINID::20080825>>
DN PREV200400023668
TI Role of narK2X and ***narGHJI*** in hypoxic upregulation of nitrate reduction by Mycobacterium tuberculosis.
AU Sohaskey, Charles D. [Reprint Author]; Wayne, Lawrence G.
CS Tuberculosis Research Laboratory (151), Department of Veterans Affairs

Medical Center, 5901 East Seventh St., Long Beach, CA, 90822, USA
chuck@sohaskey.com
SO Journal of Bacteriology, (December 2003) Vol. 185, No. 24, pp. 7247-7256. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 31 Dec 2003
Last Updated on STN: 31 Dec 2003
AB Mycobacterium tuberculosis is one of the strongest reducers of nitrate in the genus Mycobacterium. Under microaerobic conditions, whole cells exhibit upregulation of activity, producing approximately eightfold more nitrite than those of aerobic cultures of the same age. Assays of cell extracts from aerobic cultures and hypoxic cultures yielded comparable nitrate reductase activities. Mycobacterium bovis produced only low levels of nitrite, and this activity was not induced by hypoxia. M. tuberculosis has two sets of genes, ***narGHJI*** and narX of the narK2X operon, that exhibit some degree of homology to prokaryotic dissimilatory nitrate reductases. Each of these were knocked out by insertional inactivation. The narG mutant showed no nitrate reductase activity in whole culture or in cell-free assays, while the narX mutant showed wild-type levels in both assays. A knockout of the putative nitrite transporter narK2 gene produced a strain that had aerobic levels of nitrate reductase activity but failed to show hypoxic upregulation. Insertion of the M. tuberculosis ***narGHJI*** into a nitrate reductase Escherichia coli mutant allowed anaerobic growth in the presence of nitrate. Under aerobic and hypoxic conditions, transcription of ***narGHJI*** was constitutive, while the narK2X operon was induced under hypoxia, as measured with a lacZ reporter system and by quantitative real-time reverse ***PCR*** . This indicates that nitrate reductase activity in M. tuberculosis is due to the ***narGHJI*** locus with no detectable contribution from narX and that the hypoxic upregulation of activity is associated with the induction of the nitrate and nitrite transport gene narK2.
TI Role of narK2X and ***narGHJI*** in hypoxic upregulation of nitrate reduction by Mycobacterium tuberculosis.
AB. . . only low levels of nitrite, and this activity was not induced by hypoxia. M. tuberculosis has two sets of genes, ***narGHJI*** and narX of the narK2X operon, that exhibit some degree of homology to prokaryotic dissimilatory nitrate reductases. Each of these. . . strain that had aerobic levels of nitrate reductase activity but failed to show hypoxic upregulation. Insertion of the M. tuberculosis ***narGHJI*** into a nitrate reductase Escherichia coli mutant allowed anaerobic growth in the presence of nitrate. Under aerobic and hypoxic conditions, transcription of ***narGHJI*** was constitutive, while the narK2X operon was induced under hypoxia, as measured with a lacZ reporter system and by quantitative real-time reverse ***PCR*** . This indicates that nitrate reductase activity in M. tuberculosis is due to the ***narGHJI*** locus with no detectable contribution from narX and that the hypoxic upregulation of activity is associated with the induction of. . .
GEN Mycobacterium tuberculosis ***narGHJI*** gene (Mycobacteriaceae); Mycobacterium tuberculosis narK2 gene (Mycobacteriaceae); Mycobacterium tuberculosis narK2X gene (Mycobacteriaceae); Mycobacterium tuberculosis narX gene (Mycobacteriaceae)

L9 ANSWER 8 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN

DUPLICATE 5
AN 2003:445229 BIOSIS <<LOGINID::20080825>>
DN PREV200300445229
TI Genetic characterization of the nitrate reducing community based on narG nudeotide sequence analysis.
AU Cheneby, D.; Hallet, S.; Mondon, M.; Martin-Laurent, F.; Germon, J. C.; Philippot, L. [Reprint Author]
CS Microbiologie des Sols, Geosols, UMR A111, Institut National de la Recherche Agronomique, 17, Rue Sully, 21065, B.P. 86510, Dijon Cedex, France
philippo@dijon.inra.fr
SO Microbial Ecology, (July 2003) Vol. 46, No. 1, pp. 113-121. print.
ISSN: 0095-3628 (ISSN print).
DT Article
LA English
ED Entered STN: 24 Sep 2003
Last Updated on STN: 24 Sep 2003
AB The ability of facultative anerobes to respire nitrate has been ascribed mainly to the activity of a membrane-bound nitrate reductase encoded by the ***narGHJI*** operon. Respiratory nitrate reduction is the first step of the denitrification pathway, which is considered as an important soil process since it contributes to the global cycling of nitrogen. In this study, we employed direct ***PCR*** , cloning, and sequencing of narG gene fragments to determine the diversity of nitrate-reducing bacteria occurring in soil and in the maize rhizosphere. Libraries containing 727 clones in total were screened by restriction fragment analysis. Phylogenetic analysis of 128 narG sequences separated the clone families into two main groups that represent the Gram-positive and Gram-negative nitrate-reducing bacteria. Novel narG lineages that branch distinctly from all currently known membrane bound nitrate-reductase encoding genes were detected within the Gram-negative branch. All together, our results revealed a more complex nitrate-reducing community than did previous culture-based studies. A significant and consistent shift in the relative abundance of the nitrate-reducing groups within this functional community was detected in the maize rhizosphere. Thus a substantially higher abundance of the dominant clone family and a lower diversity index were observed in the rhizosphere compared to the unplanted soil, suggesting that a bacterial group has been specifically selected within the nitrate-reducing community. Furthermore, restriction fragment length polymorphism analysis of cloned narG gene fragments proved to be a powerful tool in evaluating the structure and the diversity of the nitrate-reducing community and community shifts therein.
AB. . . facultative anerobes to respire nitrate has been ascribed mainly to the activity of a membrane-bound nitrate reductase encoded by the ***narGHJI*** operon. Respiratory nitrate reduction is the first step of the denitrification pathway, which is considered as an important soil process since it contributes to the global cycling of nitrogen. In this study, we employed direct ***PCR*** , cloning, and sequencing of narG gene fragments to determine the diversity of nitrate-reducing bacteria occurring in soil and in the. . .
IT Methods & Equipment
PCR [polymerase chain reaction]: genetic techniques, laboratory techniques; cloning: genetic techniques, laboratory techniques; nucleotide sequence analysis: genetic techniques, laboratory techniques; phylogenetic. . .

L9 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2002:31640 CAPLUS <<LOGINID::20080825>>
DN 136:97395
TI Endogenous promoters and nucleic acid coding regions for gene expression and metabolic monitoring in Bacillus species
IN Bedzyk, Laura A.; Wang, Tao; Ye, Rick W.
PA E. I. Du Pont de Nemours & Co., USA
SO PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002002766	A2	20020110	WO 2001-US20873	20010629
	WO 2002002766	A3	20030109		
	W: CA, JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
	US 20020155612	A1	20021024	US 2001-891641	20010626
	US 6617148	B2	20030909		
	CA 2406643	A1	20020110	CA 2001-2406643	20010629
	EP 1294909	A2	20030326	EP 2001-957084	20010629
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
	JP 2005503752	T	20050210	JP 2002-508006	20010629
	US 20040072354	A1	20040415	US 2002-275191	20021101
	US 20040009556	A1	20040115	US 2003-602747	20030624
PRAI	US 2000-214967P	P	20000629		
	US 2001-268320P	P	20010213		
	US 2001-891641	A3	20010626		
	WO 2001-US20873	W	20010629		

AB Genes have been identified in the Bacillus genome that are responsive to various metabolic conditions and growth cycle changes. Use of the genes and their promoters for regulated gene expression in Bacillus sp. and for the monitoring of bioreactor health is claimed. A DNA microarray was constructed for Bacillus subtilis using 4,020 ***PCR*** products from oligonucleotides for all 4,100 open reading frames of the genome. CDNA probes were prepd. from total RNA isolated from B. subtilis cells and labeled with Cy3-dCTP or Cy5-dCTP. Anaerobically induced genes and their promoters were identified using RNA from exponentially-growing cells. The anaerobic growth conditions included growth with nitrate as the alternative electron acceptor, growth with nitrite, or fermentative growth without nitrate or nitrite. Gene dhb, ykuNOP, and feu regions were specifically induced in nitrite growth conditions. Similarly, RNA signals between aerobic exponential and stationary phase samples were used to identify genes and promoters induced or repressed at stationary phase in the presence of oxygen.

AB . . . sp. and for the monitoring of bioreactor health is claimed. A DNA microarray was constructed for Bacillus subtilis using 4,020 ***PCR*** products from oligonucleotides for all 4,100 open reading frames of the genome. CDNA probes were prepd. from total RNA isolated. . .

IT Operon
(***narGHJI*** , promoter and gene expression; endogenous promoters and nucleic acid coding regions for gene expression and metabolic monitoring in Bacillus species)

L9 ANSWER 10 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 2002:608150 BIOSIS <<LOGINID::20080825>>
DN PREV200200608150
TI Global gene expression analysis of Escherichia coli reveals a role for ModE-Mo in pyrimidine metabolism.
AU Hasona, A. [Reprint author]; Tao, H. [Reprint author]
CS University of Florida, Gainesville, FL, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 227. print.
Meeting Info.: 102nd General Meeting of the American Society for Microbiology. Salt Lake City, UT, USA. May 19-23, 2002. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 27 Nov 2002
Last Updated on STN: 27 Nov 2002
AB In Escherichia coli, ModE protein in association with molybdate regulates transcription of genes coding for molybdate uptake (modABC), molybdopterin synthesis (moa), fermentative dihydrogen production (hyc), nitrate reduction (narXL) and dimethyl sulfoxide reductase (dmsABC). Molybdate-dependent control of expression of nitrate reductase (***narGHJI***) and hyc also requires the product of MoeA protein. A modE, moeA double mutant of E. coli, failed to activate transcription of both ***narGHJI*** and hyc operons. To explore the role of molybdate/molybdenum, and in particular, these two proteins, in the regulation of other genes in E. coli, global gene expression profile of both a wild type and a modE, moeA double mutant, grown under anaerobic conditions, was obtained using DNA microarrays. Expression of 44 genes out of a total of 4,290 ORFs analyzed, were affected by two-fold or higher by the modE, moeA mutations. In the mutant, mRNA-derived cDNA levels were higher for 27 ORFs and lower for 17 genes. Based on this analysis, expression of the genes coding for pyrimidine degradation, deoCABD, was elevated in the double mutant while that of the pyrimidine biosynthetic genes pyrB and pyrI was higher in the isogenic parent. Results from quantitative real-time ***PCR*** experiments are in agreement with the above gene array data. A DNA sequence similar to the ModE-Mo binding sequence was also found in the Operator/promoter region of both pyrBI and deo operons. In vitro electrophoretic mobility shift experiments confirmed the binding of ModE-Mo to the operator/promoter regions of the two operons apparently to the ModE-Mo consensus sequence. These results suggest that molybdate/molybdenum plays a role in maintaining pyrimidine pool levels in the cell by activating pyrimidine biosynthesis and minimizing degradation.
AB. . . (moa), fermentative dihydrogen production (hyc), nitrate reduction (narXL) and dimethyl sulfoxide reductase (dmsABC). Molybdate-dependent control of expression of nitrate reductase (***narGHJI***) and hyc also requires the product of MoeA protein. A modE, moeA double mutant of E. coli, failed to activate transcription of both ***narGHJI*** and hyc operons. To explore the role of molybdate/molybdenum, and in particular, these two proteins, in the regulation of other. . . while that of the pyrimidine biosynthetic genes pyrB and pyrI was higher in the isogenic parent. Results from quantitative real-time ***PCR*** experiments are in agreement with the above gene array data. A DNA sequence similar to the ModE-Mo binding sequence was. . .